AU 1806

*INPUT SET: S6568.raw*

ENTERED

```
 1                              SEQUENCE LISTING
 2
 3   (1)    General Information:
 4
 5      (i) APPLICANT: Le, Junming
 6                     Vilcek, Jan
 7                     Daddona, Peter E.
 8                     Ghrayeb, John
 9                     Knight, David M.
10                     Siegel, Scott A.
11
12     (ii) TITLE OF INVENTION: MONOCLONAL AND CHIMERIC ANTIBODIES
13             SPECIFIC FOR HUMAN TUMOR NECROSIS FACTOR
14
15    (iii) NUMBER OF SEQUENCES: 5
16
17     (iv) CORRESPONDENCE ADDRESS:
18          (A) ADDRESSEE: Browdy and Neimark
19          (B) STREET: 419 Seventh Street, N.W.
20          (C) CITY: Washington
21          (D) STATE: D.C.
22          (E) COUNTRY: USA
23          (F) ZIP: 20004
24
25      (v) COMPUTER READABLE FORM:
26          (A) MEDIUM TYPE: Floppy disk
27          (B) COMPUTER: IBM PC compatible
28          (C) OPERATING SYSTEM: PC-DOS/MS-DOS
29          (D) SOFTWARE: PatentIn Release #1.0,
30        Version #1.25
31
32     (vi) CURRENT APPLICATION DATA:
33          (A) APPLICATION NUMBER:  08/013,413
34          (B) FILING DATE: 02-FEB-1993
35          (C) CLASSIFICATION: 436
36
37    (vii) PRIOR APPLICATION DATA:
38          (A) APPLICATION NUMBER: US 07/943,852
39          (B) FILING DATE: 11-SEP-1992
40
41    (vii) PRIOR APPLICATION DATA:
42          (A) APPLICATION NUMBER: US 07/853,606
43          (B) FILING DATE: 18-MAR-1992
44
45    (vii) PRIOR APPLICATION DATA:
46          (A) APPLICATION NUMBER: US 07/670,827
47          (B) FILING DATE: 18-MAR-1991
48
49     (ix) TELECOMMUNICATION INFORMATION:
50          (A) TELEPHONE: 202-628-5197
51          (B) TELEFAX: 202-737-3528
```

```
52
53
54   (2) INFORMATION FOR SEQ ID NO:1:
55
56        (i) SEQUENCE CHARACTERISTICS:
57             (A) LENGTH: 157 amino acids
58             (B) TYPE: amino acid
59             (D) TOPOLOGY: linear
60
61       (ii) MOLECULE TYPE: peptide
62
63       (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:
64
65        Val Arg Ser Ser Ser Arg Thr Pro Ser Asp Lys Pro Val Ala His Val
66        1               5                   10                  15
67
68        Val Ala Asn Pro Gln Ala Glu Gly Gln Leu Gln Trp Leu Asn Arg Arg
69                    20                  25                  30
70
71        Ala Asn Ala Leu Leu Ala Asn Gly Val Glu Leu Arg Asp Asn Gln Leu
72                    35                  40                  45
73
74        Val Val Pro Ser Glu Gly Leu Tyr Leu Ile Tyr Ser Gln Val Leu Phe
75            50                  55                  60
76
77        Lys Gly Gln Gly Cys Pro Ser Thr His Val Leu Leu Thr His Thr Ile
78        65                  70                  75                  80
79
80        Ser Arg Ile Ala Val Ser Tyr Gln Thr Lys Val Asn Leu Leu Ser Ala
81                        85                  90                  95
82
83        Ile Lys Ser Pro Cys Gln Arg Glu Thr Pro Glu Gly Ala Glu Ala Lys
84                    100                 105                 110
85
86        Pro Trp Tyr Glu Pro Ile Tyr Leu Gly Gly Val Phe Gln Leu Glu Lys
87                115                 120                 125
88
89        Gly Asp Arg Leu Ser Ala Glu Ile Asn Arg Pro Asp Tyr Leu Asp Phe
90            130                 135                 140
91
92        Ala Glu Ser Gly Gln Val Tyr Phe Gly Ile Ile Ala Leu
93        145          `        150                 155
94
95
96   (2) INFORMATION FOR SEQ ID NO:2:
97
98        (i) SEQUENCE CHARACTERISTICS:
99             (A) LENGTH: 321 base pairs
100            (B) TYPE: nucleic acid
101            (C) STRANDEDNESS: single
102            (D) TOPOLOGY: linear
```

```
103
104        (ii) MOLECULE TYPE: cDNA
105
106
107        (ix) FEATURE:
108             (A) NAME/KEY: CDS
109             (B) LOCATION: 1..321
110
111
112        (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:
113
114   GAC ATC TTG CTG ACT CAG TCT CCA GCC ATC CTG TCT GTG AGT CCA GGA    48
115   Asp Ile Leu Leu Thr Gln Ser Pro Ala Ile Leu Ser Val Ser Pro Gly
116    1               5                  10                  15
117
118   GAA AGA GTC AGT TTC TCC TGC AGG GCC AGT CAG TTC GTT GGC TCA AGC    96
119   Glu Arg Val Ser Phe Ser Cys Arg Ala Ser Gln Phe Val Gly Ser Ser
120                20                  25                  30
121
122   ATC CAC TGG TAT CAG CAA AGA ACA AAT GGT TCT CCA AGG CTT CTC ATA   144
123   Ile His Trp Tyr Gln Gln Arg Thr Asn Gly Ser Pro Arg Leu Leu Ile
124                35                  40                  45
125
126   AAG TAT GCT TCT GAG TCT ATG TCT GGG ATC CCT TCC AGG TTT AGT GGC   192
127   Lys Tyr Ala Ser Glu Ser Met Ser Gly Ile Pro Ser Arg Phe Ser Gly
128         50                  55                  60
129
130   AGT GGA TCA GGG ACA GAT TTT ACT CTT AGC ATC AAC ACT GTG GAG TCT   240
131   Ser Gly Ser Gly Thr Asp Phe Thr Leu Ser Ile Asn Thr Val Glu Ser
132    65                  70                  75                  80
133
134   GAA GAT ATT GCA GAT TAT TAC TGT CAA CAA AGT CAT AGC TGG CCA TTC   288
135   Glu Asp Ile Ala Asp Tyr Tyr Cys Gln Gln Ser His Ser Trp Pro Phe
136                85                  90                  95
137
138   ACG TTC GGC TCG GGG ACA AAT TTG GAA GTA AAA                       321
139   Thr Phe Gly Ser Gly Thr Asn Leu Glu Val Lys
140                100                 105
141
142
143   (2) INFORMATION FOR SEQ ID NO:3:
144
145        (i) SEQUENCE CHARACTERISTICS:
146             (A) LENGTH: 107 amino acids
147             (B) TYPE: amino acid
148             (D) TOPOLOGY: linear
149
150        (ii) MOLECULE TYPE: protein
151
152        (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:
153
```

PAGE: 4

RAW SEQUENCE LISTING
PATENT APPLICATION   US/08/013,413A

DATE: 09/17/93
TIME: 15:21:58

INPUT SET: S6568.raw

```
154     Asp Ile Leu Leu Thr Gln Ser Pro Ala Ile Leu Ser Val Ser Pro Gly
155      1               5                   10                  15
156
157     Glu Arg Val Ser Phe Ser Cys Arg Ala Ser Gln Phe Val Gly Ser Ser
158              20                  25                  30
159
160     Ile His Trp Tyr Gln Gln Arg Thr Asn Gly Ser Pro Arg Leu Leu Ile
161          35                  40                  45
162
163     Lys Tyr Ala Ser Glu Ser Met Ser Gly Ile Pro Ser Arg Phe Ser Gly
164          50                  55                  60
165
166     Ser Gly Ser Gly Thr Asp Phe Thr Leu Ser Ile Asn Thr Val Glu Ser
167      65                  70                  75                  80
168
169     Glu Asp Ile Ala Asp Tyr Tyr Cys Gln Gln Ser His Ser Trp Pro Phe
170                  85                  90                   95
171
172     Thr Phe Gly Ser Gly Thr Asn Leu Glu Val Lys
173                  100             105
174
175     (2) INFORMATION FOR SEQ ID NO:4:
176
177         (i) SEQUENCE CHARACTERISTICS:
178             (A) LENGTH: 357 base pairs
179             (B) TYPE: nucleic acid
180             (C) STRANDEDNESS: single
181             (D) TOPOLOGY: linear
182
183         (ii) MOLECULE TYPE: cDNA
184
185
186         (ix) FEATURE:
187             (A) NAME/KEY: CDS
188             (B) LOCATION: 1..357
189
190
191         (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:
192
193     GAA GTG AAG CTT GAG GAG TCT GGA GGA GGC TTG GTG CAA CCT GGA GGA    48
194     Glu Val Lys Leu Glu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
195      1               5                   10                  15
196
197     TCC ATG AAA CTC TCC TGT GTT GCC TCT GGA TTC ATT TTC AGT AAC CAC    96
198     Ser Met Lys Leu Ser Cys Val Ala Ser Gly Phe Ile Phe Ser Asn His
199              20                  25                  30
200
201     TGG ATG AAC TGG GTC CGC CAG TCT CCA GAG AAG GGG CTT GAG TGG GTT   144
202     Trp Met Asn Trp Val Arg Gln Ser Pro Glu Lys Gly Leu Glu Trp Val
203          35                  40                  45
204
```

```
205     GCT GAA ATT AGA TCA AAA TCT ATT AAT TCT GCA ACA CAT TAT GCG GAG   192
206     Ala Glu Ile Arg Ser Lys Ser Ile Asn Ser Ala Thr His Tyr Ala Glu
207          50              55              60
208

209     TCT GTG AAA GGG AGG TTC ACC ATC TCA AGA GAT GAT TCC AAA AGT GCT   240
210     Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Ser Ala
211      65              70              75              80
212

213     GTC TAC CTG CAA ATG ACC GAC TTA AGA ACT GAA GAC ACT GGC GTT TAT   288
214     Val Tyr Leu Gln Met Thr Asp Leu Arg Thr Glu Asp Thr Gly Val Tyr
215                  85              90              95
216
217
218

219     TAC TGT TCC AGG AAT TAC TAC GGT AGT ACC TAC GAC TAC TGG GGC CAA   336
220     Tyr Cys Ser Arg Asn Tyr Tyr Gly Ser Thr Tyr Asp Tyr Trp Gly Gln
221                  100             105             110
222

223     GGC ACC ACT CTC ACA GTC TCC                                      357
224     Gly Thr Thr Leu Thr Val Ser
225              115
226
227

228     (2) INFORMATION FOR SEQ ID NO:5:
229
230          (i) SEQUENCE CHARACTERISTICS:
231              (A) LENGTH: 119 amino acids
232              (B) TYPE: amino acid
233              (D) TOPOLOGY: linear
234
235          (ii) MOLECULE TYPE: protein
236
237          (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:
238
239     Glu Val Lys Leu Glu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
240      1               5               10              15
241

242     Ser Met Lys Leu Ser Cys Val Ala Ser Gly Phe Ile Phe Ser Asn His
243                  20              25              30
244

245     Trp Met Asn Trp Val Arg Gln Ser Pro Glu Lys Gly Leu Glu Trp Val
246              35              40              45
247

248     Ala Glu Ile Arg Ser Lys Ser Ile Asn Ser Ala Thr His Tyr Ala Glu
249          50              55              60
250

251     Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Ser Ala
252      65              70              75              80
253

254     Val Tyr Leu Gln Met Thr Asp Leu Arg Thr Glu Asp Thr Gly Val Tyr
255                  85              90              95
```

```
256
257    Tyr Cys Ser Arg Asn Tyr Tyr Gly Ser Thr Tyr Asp Tyr Trp Gly Gln
258            100             105             110
259
260    Gly Thr Thr Leu Thr Val Ser
261            115
262
```

**SEQUENCE VERIFICATION REPORT**
**PATENT APPLICATION** *US/08/013,413A*

*INPUT SET: S6568.raw*

Line                Error                                    Original Text

**SEQUENCE MISSING ITEM REPORT**
**PATENT APPLICATION  *US/08/013,413A***

*INPUT SET: S6568.raw*


< < THERE ARE NO ITEMS MISSING  > >

**SEQUENCE CORRECTION REPORT**
**PATENT APPLICATION   *US/08/013,413A***

*INPUT SET: S6568.raw*

| Line | Original Text | Corrected Text |
|------|---------------|----------------|